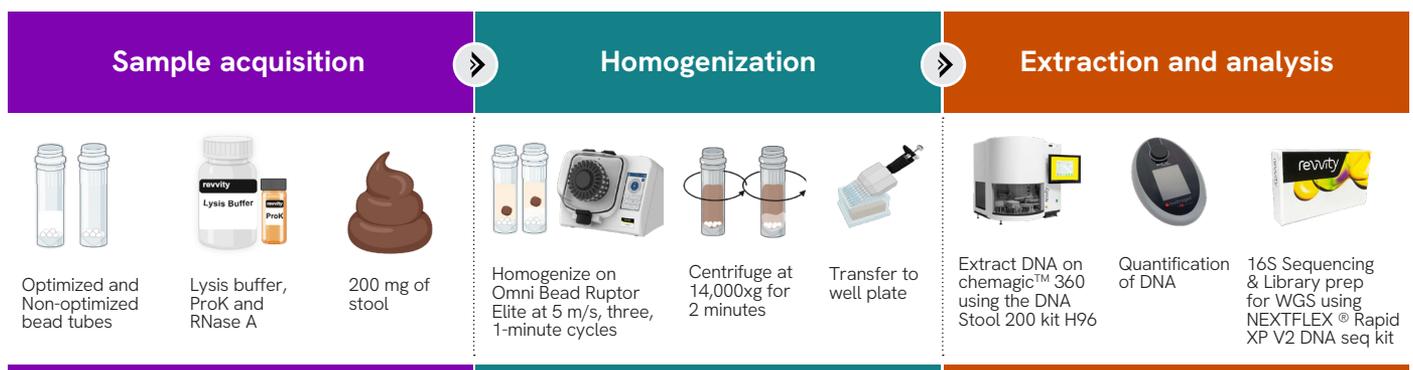# revvity

Streamline metagenomic workflows.

Stool is an established, non-invasive sample type for microbiome research, offering insight into gut health, disease mechanisms, and host–microbe interactions. However, the variability in stool consistency and microbial composition—along with the presence of PCR inhibitors—makes DNA extraction particularly challenging. Especially in high throughout laboratories.

To address these issues, we present a streamlined workflow combining the **Omni Bead Ruptor Elite™**, a powerful bead mill homogenizer, with the **chemagic™ 360** automated nucleic acid

extractor. This approach ensures thorough disruption of diverse microbial populations—including hard-to-lyse organisms—ensuring accurate representation of the gut microbiome in downstream analysis.

Bead milling delivers consistent, high-energy disruption across diverse stool matrices, improving DNA yield and quality. The resulting purified DNA is inhibitor-free and suitable for both **whole genome sequencing (WGS)** and **16S rRNA gene sequencing**, enabling comprehensive microbiome profiling.

| Sample acquisition			Homogenization			Extraction and analysis		
Optimized and Non-optimized bead tubes	Lysis buffer, ProK and RNase A	200 mg of stool	Homogenize on Omni Bead Ruptor Elite at 5 m/s, three, 1-minute cycles	Centrifuge at 14,000xg for 2 minutes	Transfer to well plate	Extract DNA on chemagic™ 360 using the DNA Stool 200 kit H96	Quantification of DNA	16S Sequencing & Library prep for WGS using NEXTFLEX ® Rapid XP V2 DNA seq kit

Metagenomic workflow for stool samples, including sample homogenization, nucleic acid extraction, library prep for whole genome sequencing (WGS) and 16S sequencing.

- Optimized bead beating yielded ~2.5× more DNA than unoptimized, showing higher sensitivity and efficiency.
- 16S sequencing revealed greater alpha diversity, enabling more comprehensive microbial profiling and reducing bias

- Unbiased extractions verified by community standard sequencing.
- WGS libraries successfully prepared and verified by QC using automated electrophoresis.

Optimzed vs non-optimized extractions based on DNA Conc.(ng/µL)
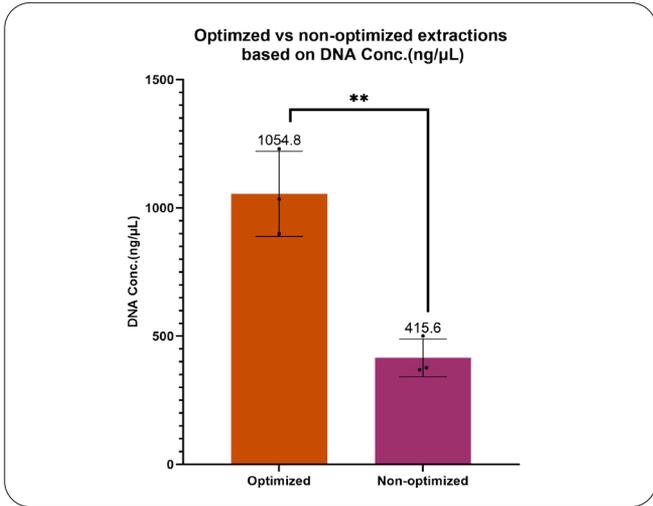
Total DNA yields from mouse stool samples after bead beating with microbiome optimized vs non-optimized bead fills.

Optimzed vs non-optimized extractions Alpha Diversity based on observed species
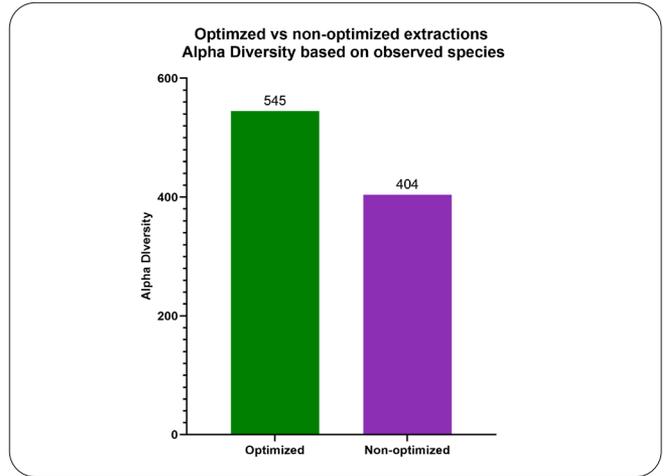
Alpha diversity comparison between optimized and non-optimized bead fill conditions, showing higher microbial species richness in optimized samples.

Comparison of nucleic acid purity ratios ($A_{280/230}$ and $A_{260/230}$) for different bead mix conditions. The non-optimized bead fill resulted in a notably lower $A_{260/230}$ ratio.
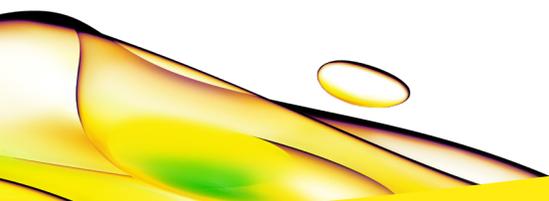
Bead mix	$A_{260/280}$	$A_{260/230}$
Non-optimized (19-628)	1.9	1.3
Microbial (19-636D)	2.0	1.7
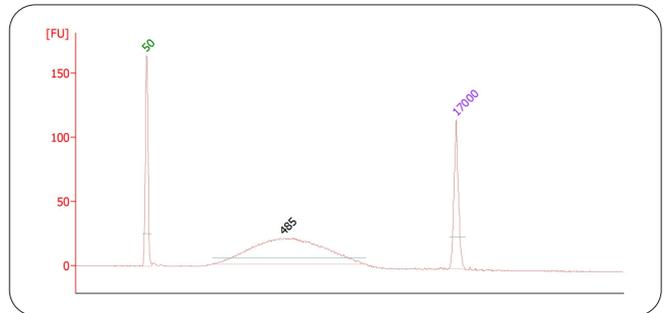
Electropherogram of WGS library prep showing a size-distributed library around 485 bp, representing sequencing-ready fragments.

Ordering info

Product	Ordering info
Omni Bead Ruptor Elite™ bead mill homogenizer	19-042E
Bead Ruptor Elite 2mL Tube Carriage (24 slots)	19-373
Microbiome Homogenizing Bead Mix (50 x 2mL tubes)	19-636D
chemagic™ 360 instrument	2024-0020
chemagic™ 96 rod head set	CMG-370
NEXTFLEX® Rapid XP V2 DNA kit	NOVA-5149-21
chemagic™ DNA stool 200 kit H96 or chemagic™ DNA soil 250 kit H96	CMG-1076 or CMG-1054

www.revvity.com

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